EXHIBIT H

Comparison of Protein (antibody) arrays according to Minden et al versus antibody arrays of our current application/invention

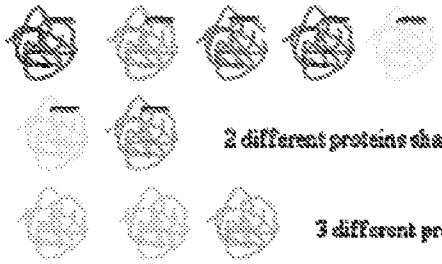
1) Reagents
2) Mindens Invention/application
3) Our invention/application
4) Comparison

Reagents

Antibodies: Two specific antibodies, antibody A and B, each recognizing a unique binding motif (motifs a and b).

antibody A  antibody B 

Sample: A heterogeneous mixture of 10 proteins (colour coded).
5 of 10 proteins carry the same binding motif (motif a - red) recognized by antibody A.
2 of 10 proteins carry the same binding motif (motif b - purple) recognized by antibody B.
3 of 10 proteins does not carry any binding motifs recognized by the antibodies

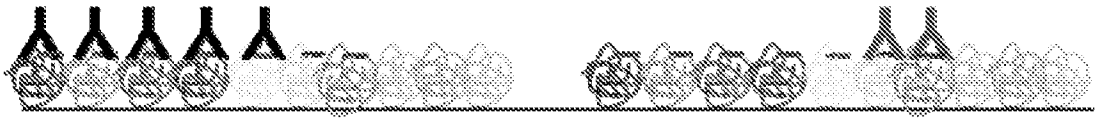


Mindens invention approach

Step 1

Spot 1 containing the deposited sample — Spot 2 containing the deposited sample

Step 2



Spot 1 containing the deposited sample — Spot 2 containing the deposited sample

Step 3

Detection
Any antibody bound to the spot will be detected
-Antibody A bound spot 1

Detection
Any antibody bound to the spot will be detected
-Antibody B bound spot 2

Step 4-5

No information of which motif-containing peptide/protein that were that were present in the sample will be obtained. In other words, the data from spot 1 will state that antibody A bound to the spot, it will not state whether it bound the black, light blue, green, dark blue or yellow ecs protein, or any combination thereof. Similar information will be obtained for spot 2.
Hence, the composition of the sample cannot be determined.

Current invention approach

Step 1

Spot 1 containing Antibody A | Spot 2 containing Antibody B

Step 2

Spot 1 containing Antibody A | Spot 2 containing Antibody B

Step 3

Detection
Any bound peptides/proteins will be detected
-5 different proteins bound in spot 1
-The 5 bound proteins are identified

Detection
Any bound peptides/proteins will be detected
-2 different proteins bound in spot 2
-The 2 bound proteins are identified

Step 4-5

Direct information of which motif-containing peptides/protein that were present in the sample will be obtained. In other words, the data from spot 1 will tell which (identify) which peptides/proteins that were bound by antibody A (in any combination). Similar information will be obtained from spot 2. Hence, the composition of the sample can be determined.

Mindens invention approach

1. The sample is (digested) and deposited in unqiue spots on the surface.

2. The antibodies are added in solution, one-by-one, and if the binding motif is present, the ab will specifically bind.

3 The bound antibodies are detected (using Nelson and/or Barry).

4. The output will simply be information on wether the ab had bound to the spot, and potentially which ab bound to which spot. It will NOT give any information to which motif containing peptide(s) the ab bound to. Hence, no information will be generated regarding the composition of the sample

5. The approach will only give information on whether the ab bound to the spot or not. As soon as 2 or more proteins per spot are deposited, the antibody binding patterns will not reveal from which protein the motif-containing peptide(s) originated, and thus not provide any information about the sample composition.

Hence, this approach is conceptually different from our invetion and NOT interchangeable. This should be evious to a skilled person.

Current invention approach

1. The antibodies are deposited in unique spots on the surface.

2. The sample is digested and added to the surface. Any motif-containing peptides will be specifically bound by the antibodies.

3. Using MS-MS, the motif-containing peptides will then be detected and identified (sequence). Based on this information, the wild type protein from which the motif containing peptides originated can be identified. Hence, detailed information about the composition of the sample will be generated.

4. Information of the sample composition can be generated for samples composed of several proteins, ranging from one to numerous (2, 10, 50, 100, 1000 etc).